

SEQUENCE LISTING

<110> Crucell Holland B.V.

Bakker, Alexander B.H.

Meester-Rood, Pauline M.L.

Bakker, Adrianus Q.

<120> AGONISTIC BINDING MOLECULES TO THE HUMAN OX40 RECEPTOR

<130> 0077 WO 00 ORD

<150> PCT/NL02/00389

<151> 2002-06-13

<160> 54

<170> PatentIn version 3.1

<210> 1

<211> 769

<212> DNA

<213> Artificial sequence

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<223> scFv SC02008

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<221> CDS

<222> (3)..(767)

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Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
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 Ser Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
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 gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca 191
 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
 50 55 60
 gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac 239
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 65 70 75
 acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg 287
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 80 85 90 95
 tat tac tgt gcc aaa gac cgc tac tcc cag gtg cac tac gcg ttg gat 335
 Tyr Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp
 100 105 110
 tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt 383
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly
 115 120 125
 tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag 431
 Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln
 130 135 140
 atg acg cag tct cca gac tca ctg ccc gtc acc cct gga gag ccg gcc 479
 Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
 145 150 155
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 160 165 170 175
 aac tat ttg gat tgg tac ctg cag aag gca ggg cag tct cca cag ctc 575
 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu
 180 185 190
 ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc 623
 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 195 200 205
 agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg 671
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 210 215 220
 gag gct gag gat gtt ggg gtt tat tac tgc cag cag tac tac aac cac 719
 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His
 225 230 235
 ccg acg acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc gcg gcc 767
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<213> Artificial sequence

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Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
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Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95

Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser
 115 120 125

Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met
 130 135 140

Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser
 145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn
 165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu Leu
 180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser
 195 200 205

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu
 210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His Pro
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<222> (3)..(773)

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cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc	95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
20 25 30	
agc ggc tac tct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg	143
Ser Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
35 40 45	
gag tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa	191
Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu	
50 55 60	
tac gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca	239
Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser	
65 70 75	
aag aac tca ctg tat ctg caa atg aac agt ctg aga gcc gag gac aca	287
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr	
80 85 90 95	
gcc gtg tat tac tgt gcc aaa gac cgc tac gtc aac acg tcg aac gcg	335
Ala Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala	
100 105 110	
ttc gat tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc	383
Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr	
115 120 125	
gga ggt tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac	431
Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp	
130 135 140	
atc cag atg aca cag tct cca gac tca ctg ccc gtc acc cct gga gag	479
Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu	
145 150 155	

ccg gcc tcc atc tcc tgc aga tct agt cag agc ctc ctg cat agt aat 527
 Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn
 160 165 170 175
 gga tac aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct cca 575
 Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
 180 185 190
 cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac 623
 Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp
 195 200 205
 agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc 671
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
 210 215 220
 aga gtg gag gct cac cat gtt ggg gtt tat tac tgc cag cag tac ccg 719
 Arg Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro
 225 230 235
 ctg ggc ccg ccc acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc 767
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<213> Artificial sequence

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Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30

Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
 50 55 60

Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
 65 70 75 80

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala Phe
 100 105 110
 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
 115 120 125
 Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile
 130 135 140
 Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro
 145 150 155 160
 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
 165 170 175
 Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
 180 185 190
 Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg
 195 200 205
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
 210 215 220
 Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro Leu
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<211> 736

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<222> (3) .. (734)

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cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc      95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    20             25             30

agc ggc tac cct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg      143
Ser Gly Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    35             40             45

gag tgg gtg gca gtt ata tca tat gat gga agt aat aaa tac tac gca      191
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
    50             55             60

gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac      239
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    65             70             75

acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg      287
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    80             85             90             95

tat tac tgt gca aga gac atg tcc ggc ttc cac gag ttc gat tac tgg      335
Tyr Tyr Cys Ala Arg Asp Met Ser Gly Phe His Glu Phe Asp Tyr Trp
    100            105            110

ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc      383
Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly
    115            120            125

gga acc ggg tct ggg act ggt acg agc gag ctc acc cag tct cca tcc      431
Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser
    130            135            140

tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca      479
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
    145            150            155

agt cag agc att agc agc tac tta aat tgg tat cag cag aaa cca ggg      527
Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
    160            165            170            175

aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt ggg      575
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
    180            185            190

gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc      623
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    195            200            205

acc atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa      671
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210            215            220

cag agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag      719
Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
    225            230            235

atc aaa cgt gcg gcc gc
Ile Lys Arg Ala Ala
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736

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<210> 6

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<213> Artificial sequence

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Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30

Gly Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95

Tyr Cys Ala Arg Asp Met Ser Gly Phe His Glu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
 115 120 125

Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser
 130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 145 150 155 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
 165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
 180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
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Lys Arg Ala Ala

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cct ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc	95
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
20 25 30	
agc gac tac acg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg	143
Ser Asp Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
35 40 45	
gag tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc	191
Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser	
50 55 60	
agg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg	239
Arg Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu	
65 70 75	
tat ctt caa atg aac aac ctg aga gct gag gac acg gcc gtg tat tac	287
Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr	
80 85 90 95	
tgt gca aga gac cgc tac ttc agg cag cag aac gcg ttc gat tac tgg	335
Cys Ala Arg Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr Trp	
100 105 110	
ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc	383
Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly	
115 120 125	

gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag atg act 431
 Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr
 130 135 140

cag tct cca gtc acc ctg ccc gtc acc cct gga gag ccg gcc tcc atc 479
 Gln Ser Pro Val Thr Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile
 145 150 155

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 Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
 160 165 170 175

ttg gat tgg tac ctg cag aag cca ggg cag tct cca cag ctc ctg atc 575
 Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
 180 185 190

tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc agt ggc 623
 Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
 195 200 205

agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg gag gct 671
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
 210 215 220

gag gat gtt ggg gtt tat tac tgc cag cag tac ctc acg gcc ccg ccc 719
 Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Leu Thr Ala Pro Pro
 225 230 235

acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc gcg gcc gc 763
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35 40 45

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
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ccg ggt ggc agc ctg cgc ctg agc tgc gcc gct agc ggc ttc acc ttt      95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
              20              25              30

agc aac gac tcg atg aac tgg atg cgc cag gcc ccg ggc aaa ggc ctc      143
Ser Asn Asp Ser Met Asn Trp Met Arg Gln Ala Pro Gly Lys Gly Leu
              35              40              45

gaa tgg gtg gcc aat atc aat cag gat ggc aac gaa aaa tat tac gcc      191
Glu Trp Val Ala Asn Ile Asn Gln Asp Gly Asn Glu Lys Tyr Tyr Ala
              50              55              60

gac tct gtc aaa ggc cgc ttc acc atc agt cgc gat aac tcc aaa aac      239
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    65              70              75

tcc ctg tac ctg cag atg aac agc ctg cgc gac gaa gat acc gcc ctg      287
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Leu
    80              85              90              95

tac tac tgc gca cgc gcc cgc gcc gcc ggc acc atc ttc gat tac tgg      335
Tyr Tyr Cys Ala Arg Ala Arg Ala Ala Gly Thr Ile Phe Asp Tyr Trp
              100              105              110

ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc      383
Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Ser Gly
              115              120              125

gga acc ggg tct ggg act ggt acg agc gag ctc gat atc cag atg acc      431
Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr
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cag agc ccg agt tcc ctg agc gcc tcc gtg ggc gac cgc gtg acc atc      479
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
              145              150              155

acc tgc cgc gcc agc cag aac gtc agc aac tac ctg acc tgg tac cag      527
Thr Cys Arg Ala Ser Gln Asn Val Ser Asn Tyr Leu Thr Trp Tyr Gln
    160              165              170              175

cag aaa ccg ggc aag gct ggc aaa ctg ctg att tac gcc gcc agc agc      575
Gln Lys Pro Gly Lys Ala Gly Lys Leu Leu Ile Tyr Ala Ala Ser Ser
              180              185              190

ctc caa agc ggc gtg ccg tct aga ttc agt ggc tcc ggc tcc gga acc      623
Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
              195              200              205

gat ttt acc ctg acc atc agc agc ctg cag ccg gaa gat ttc gct acc      671
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
              210              215              220

tac tat tgt cag cag tcc tac ttc aac ccg gcg acc ttc ggc cag ggc      719
Tyr Tyr Cys Gln Gln Ser Tyr Phe Asn Pro Ala Thr Phe Gly Gln Gly
              225              230              235

acc aaa ctg gaa atc aaa cgc gcg gcc gc      748
Thr Lys Leu Glu Ile Lys Arg Ala Ala
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<212> PRT

<213> Artificial sequence

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Asn Asp Ser Met Asn Trp Met Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ala Asn Ile Asn Gln Asp Gly Asn Glu Lys Tyr Tyr Ala Asp
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Leu Tyr
 85 90 95

Tyr Cys Ala Arg Ala Arg Ala Ala Gly Thr Ile Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
 115 120 125

Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr Gln
 130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 145 150 155 160

Cys Arg Ala Ser Gln Asn Val Ser Asn Tyr Leu Thr Trp Tyr Gln Gln
 165 170 175

Lys Pro Gly Lys Ala Gly Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
 180 185 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
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Tyr Cys Gln Gln Ser Tyr Phe Asn Pro Ala Thr Phe Gly Gln Gly Thr
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Lys Leu Glu Ile Lys Arg Ala Ala
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<212> DNA

<213> Artificial sequence

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<222> (3)..(767)

<223>

<400> 11

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Pro Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
20 25 30	
agc agc tac gcg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg	143
Ser Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
35 40 45	
gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac gca	191
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala	
50 55 60	
gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac	239
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn	
65 70 75	
acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg	287
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	
80 85 90 95	
tat tac tgt gcc aaa gac cgc tac atc acg ttg ccg aac gcg ttg gat	335
Tyr Tyr Cys Ala Lys Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp	
100 105 110	
tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt	383
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly	
115 120 125	

tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag 431
 Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln
 130 135 140

atg acc cag tct cca gtc tca ctg ccc gtc acc cct gga gag ccg gcc 479
 Met Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
 145 150 155

tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac 527
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
 160 165 170 175

aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct cca cag ctc 575
 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
 180 185 190

ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc 623
 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 195 200 205

agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg 671
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 210 215 220

gag gct gag gat gtt ggg gtt tat tac tgc cag cag tac aag tcg aac 719
 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Lys Ser Asn
 225 230 235

ccg ccc acc ttc ggc cag ggc acc aaa gtg gaa atc aaa cgc gcg gcc 767
 Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 240 245 250 255

gc 769

<210> 12

<211> 255

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02021

<400> 12

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15

Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30

Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Ala Lys Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser
 115 120 125
 Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met
 130 135 140
 Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser
 145 150 155 160
 Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn
 165 170 175
 Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu
 180 185 190
 Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser
 195 200 205
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu
 210 215 220
 Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Lys Ser Asn Pro
 225 230 235 240
 Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 245 250 255

<210> 13

<211> 745

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02022

<220>

<221> CDS

<222> (3) .. (743)

<223>

<400> 13

cc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cat	47
Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His	
1 5 10 15	
cct ggg ggg tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc	95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe	
20 25 30	
agt agc tat gct atg cac tgg gtt cgc cag gct cca gga aaa ggt ctg	143
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
35 40 45	
gag tgg gta tca gct att ggt acc ggt ggt ggc aca tac tat gca gac	191
Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp	
50 55 60	
tcc gtg cag ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc	239
Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser	
65 70 75	
ttg tat ctt caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat	287
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr	
80 85 90 95	
tac tgt gca aga tac gac gag ccg ctg acg att tac tgg ttt gac tcc	335
Tyr Cys Ala Arg Tyr Asp Glu Pro Leu Thr Ile Tyr Trp Phe Asp Ser	
100 105 110	
tgg ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca	383
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser	
115 120 125	
ggc gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc aca cag	431
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln	
130 135 140	
tct cca gcc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc tcc	479
Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser	
145 150 155	
tgc agg gcc agt cag agt gtt agc agc tac tta gcc tgg tac caa cag	527
Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln	
160 165 170 175	
aaa cct ggc cag gct ccc agg ctc ctc atc tat gat gca tcc aac agg	575
Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg	
180 185 190	
gcc act ggc atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac	623
Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
195 200 205	
ttc act ctc acc atc agc agc cta gag cct gaa gat ttt gca gtt tat	671
Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr	
210 215 220	
tac tgt cag cag cgt agc aac tgg cct ccg gct ttc ggc gga ggg acc	719
Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr	
225 230 235	
aag gtg gag atc aaa cgt gcg gcc gc	745
Lys Val Glu Ile Lys Arg Ala Ala	
240 245	

<210> 14

<211> 247

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02022

<400> 14

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro
 1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser
 20 25 30

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser
 50 55 60

Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
 65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg Tyr Asp Glu Pro Leu Thr Ile Tyr Trp Phe Asp Ser Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
 165 170 175

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala
 180 185 190

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 195 200 205

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
 210 215 220

Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr Lys
 225 230 235 240

Val Glu Ile Lys Arg Ala Ala
 245

<210> 15

<211> 745

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02023

<220>

<221> CDS

<222> (3)..(743)

<223>

<400> 15

cc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cat 47
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His
 1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc 95
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
 20 25 30

agt agc tat gct atg cac tgg gtt cgc cag gct cca gga aaa ggt ctg 143
 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45

gag tgg gta tca gct att ggt act ggt ggt ggc aca tac tat gca gac 191
 Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp
 50 55 60

tcc gtg atg ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg 239
 Ser Val Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75

ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat 287
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 80 85 90 95

tac tgt gca aga tac gac aat gtg atg ggt ctt tac tgg ttt gac tac 335
 Tyr Cys Ala Arg Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr
 100 105 110

tgg ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca 383

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125
 ggc gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc aca cag 431
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln
 130 135 140
 tct cca gcc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc tcc 479
 Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
 145 150 155
 tgc agg gcc agt cag agt gtt agc agc tac tta gcc tgg tac caa cag 527
 Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
 160 165 170 175
 aaa cct ggc cag gct ccc agg ctc ctc atc tat gat gca tcc aac agg 575
 Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg
 180 185 190
 gcc act ggc atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac 623
 Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205
 ttc act ctc acc atc agc agc cta gag cct gaa gat ttt gca gtt tat 671
 Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr
 210 215 220
 tac tgt cag cag cgt agc aac tgg cct ccg gct ttc ggc gga ggg acc 719
 Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr
 225 230 235
 aag gtg gag atc aaa cgt gcg gcc gc 745
 Lys Val Glu Ile Lys Arg Ala Ala
 240 245

<210> 16

<211> 247

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02023

<400> 16

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro
 1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser
 20 25 30

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser
 50 55 60

Val Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 65 70 75 80
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Ala Arg Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln Ser
 130 135 140
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160
 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
 165 170 175
 Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala
 180 185 190
 Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 195 200 205
 Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
 210 215 220
 Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr Lys
 225 230 235 240
 Val Glu Ile Lys Arg Ala Ala
 245

<210> 17

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02008

<400> 17

Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr
 1 5 10

<210> 18

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02009

<400> 18

Asp Arg Tyr Val Asn Thr Ser Asn Ala Phe Asp Tyr
1 5 10

<210> 19

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02010

<400> 19

Asp Met Ser Gly Phe His Glu Phe Asp Tyr
1 5 10

<210> 20

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02011

<400> 20

Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr
1 5 10

<210> 21

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02012

<400> 21

Ala Arg Ala Ala Gly Thr Ile Phe Asp Tyr
1 5 10

<210> 22

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02021

<400> 22

Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp Tyr
1 5 10

<210> 23

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02022

<400> 23

Tyr Asp Glu Pro Leu Thr Ile Tyr Trp Phe Asp Ser
1 5 10

<210> 24

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02023

<400> 24

Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr
 1 5 10

<210> 25

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain of 008

<400> 25

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 26

<211> 449

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain of 011

<400> 26

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 27

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain 021

<400> 27

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Arg Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 28

<211> 450

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain of 023

<400> 28

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Met
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255

 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335

 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365

 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

 Gly Lys
 450

<210> 29

<211> 219

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 008

<400> 29

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr
85 90 95

Tyr Asn His Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 30

<211> 219

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 011

<400> 30

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr
 85 90 95

Tyr Asn His Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 31

<211> 219

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 021

<400> 31

Asp Ile Gln Met Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr
 85 90 95

Lys Ser Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 32

<211> 214

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 023

<400> 32

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 33

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZalphaB

<220>

<221> CDS

<222> (1)..(54)

<223>

<400> 33

tct	ctc	gag	aaa	aga	gag	gct	gaa	gct	gca	gga	att	cac	gtg	gcc	cag	48
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Ala	Gly	Ile	His	Val	Ala	Gln	
1			5					10					15			

ccg	gcc	g														55
Pro	Ala															

<210> 34

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZalphaB

<400> 34

Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Ala	Gly	Ile	His	Val	Ala	Gln	
1			5					10					15			

Pro Ala

<210> 35

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZFVH

<220>

<221> CDS

<222> (1)..(54)

<223>

<400> 35

tct	ctc	gag	aaa	aga	gcc	atg	gaa	gct	gca	gga	att	cac	gtg	gcc	cag	48
Ser	Ieu	Glu	Lys	Arg	Ala	Met	Glu	Ala	Ala	Gly	Ile	His	Val	Ala	Gln	
1				5					10					15		

ccg	gcc	g														55
Pro	Ala															

<210> 36

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZFVH

<400> 36

Ser	Ieu	Glu	Lys	Arg	Ala	Met	Glu	Ala	Ala	Gly	Ile	His	Val	Ala	Gln	
1				5					10					15		

Pro Ala

<210> 37

<211> 92

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic hinge region

<220>

<221> CDS

<222> (1)..(90)

<223>

<400> 37

gcg gcc gcg cca aag cca agt acc cca cca ggt tct tca tgt cca cca	48
Ala Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro Pro	
1 5 10 15	

tgt cca ggc tct ggc ggt gcg cca atc gat agc ggc ttt cta ga	92
Cys Pro Gly Ser Gly Gly Ala Pro Ile Asp Ser Gly Phe Leu	
20 25 30	

<210> 38

<211> 30

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic hinge region

<400> 38

Ala Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro Pro
1 5 10 15

Cys Pro Gly Ser Gly Gly Ala Pro Ile Asp Ser Gly Phe Leu
20 25 30

<210> 39

<211> 1416

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 008

<400> 39

atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga attctccatg	60
gccgaggtgc agctggtgga gtctggggga ggcttggtcc agcctggagg gtccctgaga	120
ctctcctgtg cagcctctgg attcaccttt agcaactaca cgatgaactg ggtccgccag	180
gcgcccggga aggggctgga gtgggtctca gctattagtg gtagtggtgg tagcacatac	240
tacgcagact ccgtgaaggg ccggttcacc atctccagag acaattccaa gaacacgctg	300
tatctgcaaa tgaacagcct gagagccgag gacacggccg tgtattactg tgccaaagac	360

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cgctactccc aggtgcacta cgcggttgat tactggggcc agggcaccct ggtgaccgtc 420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcgggcct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac totactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagagagtt 720
gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 780
gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 840
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagtgc 900
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 960
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgaccagga ctggctgaat 1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1080
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
cccgtgctgg actccgacgg ctcttcttc ctctatagca agctcaccgt ggacaagagc 1320
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
tacacgcaga agagcctctc cctgtctccg ggtaaa 1416

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<210> 40

<211> 1410

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 011

<400> 40

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atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga attctccatg 60
gccgaggtgc agctggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga 120
ctctcctgtg cagcctctgg attcaccttc agcgactaca cgatgaactg ggtccgccag 180
gcgccccgga aggggctgga gtgggtctca tccattagt gtggtagcac atactacgca 240
gactccagga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 300
caaatgaaca acctgagagc tgaggacacg gccgtgtatt actgtgcaag agaccgctac 360
ttcaggcagc agaacgcgtt cgattactgg ggccagggca cctggtgac cgtctcctca 420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

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ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg      540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtctca      600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc      720
aaatcttgtg acaaaactca cacatgcca cctgcccag cacctgaact cctgggggga      780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct      840
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac      960
agcacgtacc gtgtggtcag cgtcctcacc gtctcgcacc aggactggct gaatggcaag     1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag     1140
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccggtg     1260
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg     1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa cactacacg     1380
cagaagagcc tctccctgtc tccgggtaaa                                1410

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<210> 41

<211> 1416

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 021

<400> 41

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atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga attctccatg      60
gccgaggtgc agctggtgga gtctggggga ggcttggtac agcctagggg gtccctgaga     120
ctctcctgtg cagcctctgg attcaccttt agcagctacg cgatgaactg ggtccgccag     180
gcgcccggga aggggctgga gtgggtggca gttatatcat atgatggaag caataaatac     240
tacgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgtg      300
tatctgcaaa tgaacagcct gagagctgag gacacagccg tgtattactg tgccaaagac     360
cgctacatca cgttgccgaa cgcgttggtat tactggggcc agggcaccct ggtgaccgtc     420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc     480
tctgggggca cagcgccctt gggctgcctg gtcaaggact acttccccga accggtgacg     540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag     600

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tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaaag cccagcaaca ccaaggtgga caagagagtt 720
gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 780
gggggaccgt cagtcttctt cttcccccca aaaccaag acaccctcat gatctcccgg 840
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 960
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1080
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
cccgtgctgg actccgacgg ctctctcttc ctctatagca agctcaccgt ggacaagagc 1320
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
tacacgcaga agagcctctc cctgtctccg ggtaaa 1416

```

<210> 42

<211> 1413

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 023

<400> 42

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atggcatgcc ctggcttctt gtgggcactt gtgatctcca cctgtcttga attctccatg 60
gccgaggtgc agctggtgga gtctggggga ggcttggtac atcctggggg gtccctgaga 120
ctctcctgtg caggctctgg attcaccttc agtagctatg ctatgcactg ggttcgccag 180
gctccaggaa aaggtctgga gtgggtatca gctattggta ctggtggtgg cacatactat 240
gcagactccg tgatggggcc gttcaccatc tccagagaca attccaagaa cacgctgtat 300
ctgcaaataa acagcctgag agccgaggac acggccgtgt attactgtgc aagatacgac 360
aatgtgatgg gtctttactg gtttgactac tggggccagg gcaccctggt gaccgtctcc 420
tcagcctcca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 480
gggggacacg cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 540
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 600
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720

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cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 780
ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccgacc 840
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 960
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1080
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgagg 1140
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccagcgac 1200
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1260
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1320
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggtctgca caaccactac 1380
acgcagaaga gcctctccct gtctccgggt aaa 1413

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<210> 43

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of light chain of 008

<400> 43

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atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtctcga gttttccatg 60
gctgacatcg tgatgacaca gtctccagac tcaactgccg tcaccctgg agagccggcc 120
tccatctcct gcaggcttag tcagagcctc ctgcatagta atggatacaa ctatttggat 180
tggtacctgc agaaggcagg gcagtctcca cagctcctga tctatttggg ttctaatacgg 240
gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 300
atcagcagag tggaggctga ggatgttggg gtttattact gccagcagta ctacaaccac 360
ccgacgacct tcggccaggg caccaaactg gaaatcaaac gtactgtggc tgcaccatct 420
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 480
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtga taacgccctc 540
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 720

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<210> 44

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of light chain of 011

<400> 44

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gctgacatcg tgatgacaca gtctccagtc accctgcccg tcacccttg agagccggcc      120
tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat      180
tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatacgg      240
gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa      300
atcagcagag tggaggctga ggatgttggg gtttattact gccagcagta cctcacggcc      360
ccgccacct tcggccaggg caccaaactg gaaatcaaac gtactgtggc tgcaccatct      420
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc      480
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc      540
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      600
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      660
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      720

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<210> 45

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of light chain of 021

<400> 45

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atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtctcga gttttccatg      60
gctgacatcc agatgaccca gtctccagtc tcaactgccc tcacccttg agagccggcc      120
tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat      180
tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatacgg      240
gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa      300
atcagcagag tggaggctga ggatgttggg gtttattact gccagcagta caagtcgaac      360
ccgccacct tcggccaggg caccaaagtg gaaatcaaac gtactgtggc tgcaccatct      420
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc      480

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ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 540
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600
 ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 720

<210> 46

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of light chain of 023

<400> 46
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 gctgaaattg tgctcacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 120
 accctctcct gcagggccag tcagagtgtt agcagctact tagcctggta ccaacagaaa 180
 cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 240
 gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag 300
 cctgaagatt ttgcagtta ttactgtcag cagcgtagca actggcctcc ggctttcggc 360
 ggagggacca aggtggagat caaacgtact gtggctgcac catctgtctt catcttcccg 420
 ccattctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480
 tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggttaactcc 540
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctcg 600
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 660
 ggctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

<210> 47

<211> 46

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 47
 acctgtcttg aattctccat ggccgaggtg cagctgggtg agtctg 46

<210> 48

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 48

gctcgcggat ccactcacct gaggagacgg tcaccagggt gccctggccc c

51

<210> 49

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 49

acctgtctcg agttttccat ggctgacatc gtgatgacac agtctccag

49

<210> 50

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 50

acctgtctcg agttttccat ggctgacatc gtgatgaccc agtctcc

47

<210> 51

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 51
acctgtctcg agttttccat ggctgaaatt gtgctcacac agtctccagc cacc 54

<210> 52

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 52
ttttccttag cggccgcaaa gtgcacttac gtttgatttc cagtttggtg ccctg 55

<210> 53

<211> 55

<212> DNA

<213> Artificial sequence

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